Listing of the Claims

This listing of claims will replace all prior versions, and listings, of claims in the application:

1. (Previously presented) A method for determining a haplotype of a subject comprising the steps of:
   (a) diluting a nucleic acid sample from the subject into a single molecule dilution;
   (b) amplifying the diluted single molecule dilution in a multiplex amplification reaction with at least four different primer pairs designed to amplify at least four nucleic acid regions each comprising at least one polymorphic site;
   (c) genotyping the at least four nucleic acid regions wherein each region contains at least one polymorphic site wherein the genotyping is performed using primer extension and mass spectrometric detection;
   (d) repeating steps a-c from the same nucleic acid sample to obtain 12-18 genotype replicas from the same subject and thereafter comparing the at least 12-18 genotype replicas to determine the haplotype; and
   (e) determining the haplotype from the genotypes of the at least four polymorphic sites to obtain a haplotype for the subject.
2. (Cancelled)
3. (Previously presented) The method of claim 1, further comprising comparing the haplotype with a haplotype from a control or a database of haplotypes from controls to determine association of the haplotype with a biological trait.
4. (Currently amended) ~~The method of claim 1~~, A method for determining a haplotype of a subject comprising the steps of:
   (a) diluting a nucleic acid sample from the subject into a single molecule dilution;

(b) amplifying the diluted single molecule dilution in a multiplex amplification reaction with at least four different primer pairs designed to amplify at least four nucleic acid regions each comprising at least one polymorphic site;

(c) genotyping the at least four nucleic acid regions wherein each region contains at least one polymorphic site wherein the genotyping is performed using primer extension and mass spectrometric detection;

(d) repeating steps a-c from the same nucleic acid sample to obtain 12-18 genotype replicas from the same subject and thereafter comparing the at least 12-18 genotype replicas to determine the haplotype; and

(e) determining the haplotype from the genotypes of the at least four polymorphic sites to obtain a haplotype for the subject,

wherein the at least four polymorphic sites contain a polymorphism that is a single nucleotide polymorphism.

5. (Previously presented) The method of claim 1, wherein the at least four polymorphic sites contain a polymorphism selected from a deletion, an insertion, a substitution or an inversion.

6. (Previously presented) The method of claim 1, wherein the at least four polymorphic sites contain a polymorphism wherein each of the polymorphisms is selected from the group consisting of a single nucleotide polymorphism, deletion, an insertion, a substitution or an inversion.

7.-8. (Cancelled)

9. (Previously presented) A method of diagnosing a disease condition or disease susceptibility by determining a disease related haplotype in a subject comprising the steps of:

(a) diluting a nucleic acid sample from the subject into a single molecule dilution;

(b) amplifying the diluted single molecule dilution [[and]] in a multiplex amplification reaction with at least two primer pairs designed to amplify a region comprising at least two polymorphic sites in the nucleic acid template;

(c) genotyping the polymorphic sites in the single nucleic acid molecule wherein the genotyping is performed using primer extension and mass spectrometric detection;

(d) repeating steps a-c from the same nucleic acid sample to obtain 12-18 genotype replicas from the same subject and thereafter comparing the at least 12-18 genotype replicas to determine the haplotype;

(e) determining the haplotype from the genotype of at least two polymorphic sites to obtain a haplotype for the subject; and

(f) comparing the haplotype of the subject to known disease-associated haplotypes, wherein a match in the sample haplotype with a disease-associated haplotype indicates that the subject has the disease or that the subject is susceptible for the disease.

10.-11. (Cancelled)

12. (Previously presented) A method of determining a haplotype of a subject comprising the steps of:

(a) treating a nucleic acid sample from the subject with a composition that differentially affects an epigenetically modified nucleotide in the nucleic acid sample to effectively create polymorphisms based on the epigenetic modification;

(b) diluting the treated nucleic acid sample into a single copy dilution;

(c) amplifying the diluted nucleic acid sample using at least four different primer pairs in a multiplex amplification reaction;

(d) genotyping the amplified sample, wherein genotyping is performed using primer extension and mass spectrometric detection;

(e) repeating steps b-c from the same treated nucleic acid sample to obtain 12-18 genotype replicas from the same subject and thereafter comparing the at least 12-18 genotype replicas; and

(f) determining the haplotype of the subject from the genotyped sample.

13.-14. (Cancelled)

15. (Original) The method of claim 12, wherein the epigenetically modified nucleotide is a methylated nucleotide.

16. (Original) The method of claim 15, wherein the nucleic acid sample is treated with bisulfite.

17. (Currently amended) A method of determining a haplotype in a subject comprising the steps of:

(a) digesting a nucleic acid sample from the subject with a methylation-sensitive restriction enzyme so that either unmethylated DNA or methylated DNA is left intact, depending on which enzyme is used;

(b) diluting the digested nucleic acid sample to a single molecule concentration;

(c) amplifying the diluted and ~~undiluted~~ digested nucleic acid sample with at least two different primer pairs in a multiplex amplification reaction;

(d) genotyping the amplified samples, wherein genotyping is performed using primer extension and mass spectrometric detection;

(e) repeating steps b-c from the same treated nucleic acid sample to obtain 12-18 genotype replicas from the same subject and thereafter comparing the at least 12-18 genotype replicas; and

(f) determining a haplotype of a methylated nucleic acid wherein at least one polymorphic marker next to the methylation site, together with the methylation site, constitutes a haplotype.

18.-19. (Cancelled)

20. (New) The method of claim 1, 4, 9, 12 or 17, wherein the primer pairs amplify a short amplicon of about 50 to about 100 base pairs.